

Amendments to the Specification:

Insert the following paragraph at page 1, immediately below the title of the application:

**CROSS REFERENCE TO RELATED APPLICATIONS**

--This application is a divisional (and claims the benefit of priority under 35 USC 120) of U.S. application serial no. 09/684,579, filed October 6, 2000, which claims priority to and is a continuation-in-part of PCT/JP99/01913, filed April 9, 1999, which claims priority from Japanese Application 10/115975, filed April 10, 1998. The disclosures of the prior applications are considered part of (and are incorporated by reference in) the disclosure of this application.--

Replace the paragraph beginning at page 7, line 1, with the following paragraph:

--It is also well within the art of a person with ordinary skill to obtain a protein functionally equivalent to the mouse striamin protein (SEQ ID NO:1) by isolating DNA showing significant homology with the DNA that encodes the mouse striamin protein (SEQ ID NO:2) or a part thereof, using technology such as a hybridization technique (Sambrook et al., Molecular Cloning 2nd ed. 9.47-9.58, Cold Spring Harbor Lab. Press, 1989). Thus, the proteins of the present invention also include those proteins that are encoded by DNA hybridizing with the DNA encoding the mouse striamin protein, and that are functionally equivalent to the mouse striamin protein (e.g., the protein that was detected in Example 5, which is encoded by a human transcript 3.1 kb in length). When hybridizing DNA is isolated from other organisms, animals including, but not limited to, humans, rats, rabbits, and cattle are used for the isolation. For this purpose, tissues such as skeletal muscles, in particular, are suitable. DNAs thus isolated, which encode proteins functionally equivalent to the mouse striamin protein, generally show significant homology with the DNA (SEQ ID NO:2) encoding the mouse striamin protein (SEQ ID NO:1). The term "significant homology" indicates a sequence identity of at least 40%, preferably at least 60%, more preferably at least 80%, and most preferably at least 95% at amino acid level. The degree of homology can be determined according to the algorithm described in the literature (Wilbur, W. J. and Lipman, D. J. Proc. Natl. Acad. Sci. USA (1983), 80:726-730).--

Replace the paragraph beginning at page 7, lines 19-29, with the following rewritten paragraph:

-- The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3. Where gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. The programs are available at the web site of the National Center for Biotechnology Information.--

Replace the abstract at page 39 with the following amended abstract:

--The invention relates to a novel nucleic acid sequence encoding a polypeptide expressed in immortalized cells. The polypeptide is expressed in skeletal muscles and undifferentiated cells. The polypeptide encoded by the nucleic acid sequence inhibits the differentiation of myoblasts into myotubes.--